

Fig. 1



Fig.

Fig. 2



ICTB : 471	TGTCAGTGTCTACGGCCCTCAACCAATGGATCTACGGCGTTGAAGAGCTGGCGACTTGGGT	530
SLR : 483	GGTGGGAGTTACGGTCTCGGACAAACAGGTGGACGGGTAGAACAGTTAGCCACTTGGAA	542
ICTB : 531	GGATCGCAACTCGGTTGCCGACTTCACCTCACGGGTTTACAGCTATCTGGGCAACCCCAA	590
SLR : 543	TGACCCCACTCTACCTTGGCCCAAGCCACTAGGGTATATAGCTTTTTAGGTAATCCCAA	602
ICTB : 591	CCTGCTGGCTGCTTATCTGGTGCCGACGACTGCCCTTTT-CTGCAGCAGCGCATCGGGGTGT	649
SLR : 603	TCCTTTGGCGGCTTACCTGGTGCCCAATGACGGGTTTGAGCTTGAGT-GCCCTGGTGGTAT	661
ICTB : 650	GGCGCGGCTGGCTCCCCAAGCTGCTGGCGATCG-CTGCGACAGGTGCGAGCAGCCTTATGT	708
SLR : 662	GGCGACGGTGGTGCGCCCAACTGCTGG-GAGCAACCATGGTGATTGTTAACCTACTCTGT	720
ICTB : 709	CTGATCCTCACCTACAGTCGCGGTGGCTGGCTGGTTTGTGCGCCATGATTTTGTCTGG	768
SLR : 721	CTCTTTTTTACCCAGAGCCGGGGCGGTGGCTAGCAGTGCTGGCCCTGGGAGCTACCTTC	780
ICTB : 769	GCGTTATTAGGGCTCTACTGGTTTCAACCCCGTCTACCCGACCCCTGGCGACGCTGGCTA	828
SLR : 781	CTGGCCCTTTGTACTTCTGTGTGTTACCCCAATTACCCCAATTTTGGCAACGGTGGTCT	840
ICTB : 829	TTCCCAAGTCGTATTGGGTGGACTAGTCTCGCGGTGCTCTT-GGTGGCGGTGCTTGGACT--	884
SLR : 841	TTGCCCTTGGC----GATCGCC--GTGGCGGTTATATTAGGTGGGGGAGCGTTGATTGCG	894
ICTB : 885	-TG-AGCCCGTTGCGCGTGGCGGTGTTGAGCATCTTTGTGGGGCGCTGAAGACAGCAGCAAC	942
SLR : 895	GTGGAACCGGATTCGACTCAGGGCCCATGAGCATTTTGTCTGGCGGGGAAGACAGCAGTAAT	954

Fig. 2
(Continued)



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ICTB : 943   AACTTCGGGATCAATGTCTGGCTGCCGTGCTGCAGATGATTCAAGATCCGGCCTTGGCTG 1002
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SLR  : 955   AATTTCGGCNTCAATGTTTGGGAAGGGGTAAAGCCATGATCCGAGCCCCGCCCTATCAT 1014

ICTB : 1003  GGCATCGGCCCCGGCAATACCGCCTTTAACCCTGGTTTATCCCCTCTATCAACAGCGCGC 1062
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SLR  : 1015  GGCATTGGCCCCAGGTAACGAAGCCCTTTAACCAAATTTATCCTTACTATATGCGGCCCGCC 1074

ICTB : 1063  TTTRACGGCGTTGAGCGCCTACTCCGTCGCCGTGGAAGTCGCGGTTGAGGGCGGACTACTG 1122
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SLR  : 1075  TTCACCGCCCTGAGTGCCCTATTCCCATTTACCTAGAAAATTTTGGTGAACGGGTGTAGTT 1134

ICTB : 1123  GGCTTGA-CGGCCTTCGCTTGGCTGCT-GCTGGTCACGGCGGCTGACGGCGGTGCGGCAGG 1180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SLR  : 1135  GGTTTTACCTGTATGCTC-TGGCTGTTGGCCGTTACCCCTAGGCCAAAGGC-GTAGA ACTGG 1192

ICTB : 1181  TGRGCCGAC TGCGCGCGGATCGCAATCCCC--AAGCCTTTTGGTTGATGGCTAGCTTGCC 1238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SLR  : 1193  TTAAACG-CTGTCCG-CAAAACCCTCGCCCCCGGAAGGCATCTGGATTATGGGGGCTTTAGC 1250

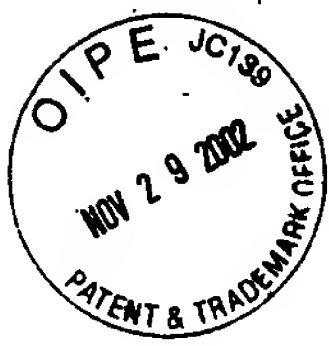
ICTB : 1239  CGGTTTGGCAGGAATGCTGSGTCACGGTCTGTTTGATACCGTGCTCTATCGACCGGAAGC 1298
      |    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SLR  : 1251  GECGATCATCGGCTTTGTTGGTCCACGGGCATGGTAGATACAGTCTGTGTA CCGTCCCCCGGT 1310

ICTB : 1299  CAGTACGCTCTGCTGGCTCTGTATTGG--AGCGATCGCGAGTTTCTGG--CAGC-CCCAA 1353
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SLR  : 1311  GAGCACCTTGTGGTGG-TTGCTAGTGGCCATTG-TTGCTAGTCA GTGGGCCAGCGCCACG 1368

ICTB : 1354  CETTCCAAGCAACTCCCTCCAGNAGCCGAGCATTCAGACGAA 1395
      |    ||||| ||||| ||||| ||||| ||||| ||||| |||||
SLR  : 1369  GCCCGTTTTGGAGGCCAGTAAGAA---GAAATGAGGACAAA 1407

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Fig. 2
(Continued)



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+++W++L F + PQ+WG S LHRL G ++W +S L   EALG L+A+++ +APF
SLR : 5  ISINRSLMFGGSPQENGRCVLRHRLVGVGWQENIQASVLRPHFEALGTALVAIFIAAPF 64

      ++ LG+ +  A+WALL+ D + TPIH LV YM + A+A G SPV+ AA G
ICTB : 61 VPSSALGLGLAIAAYWALLSLTDIDLQRQATPIHVLVLLYWGVDALATGLSPVRAALVG 120
SLR : 65 TSTTMIGIPMLLCCGAFWALLTPADQPGKGLTPIHVLVFAIYWCISAIAGVGFSPVKMAASG 124

      LAKLT L +F LAAR+L+N + + L +VV++ L V YGL Q + GVE+LATW D
ICTB : 121 LAKLTLYLLVPALAAARVLRNPRLLPSVVVITSLFVSVYGLNQMIYGVEXLATWDRN 180
SLR : 125 LAKLTANLCLFLLAARLLQNKQWLNRLVTVLLVGLLVGSYGLRQQQVDGVEQLATWDEPT 184

      S +RVYS+LGNPNLLAAYLVE T S +A+ VWR W PKLL + LCL T
ICTB : 181 SVADFTSRVSYLGNPNLLAAYLVEPTTAFSAAAIGVWRGNLPKLLAIAATGASSLCLILT 240
SLR : 185 STLAQATRVYSFLGNPNLLAAYLVEPTMTGLSLSALVVWRRWPKLLGATMVIUNLLCLFFT 244

      SRGGWL +A+ + L +W+ P+LP W+RW P+ + V + A++ +EP+R+
ICTB : 241 YSRGGWLGFWAMIFVWALLGLYHQPRLPAPWRRWLPVVLGGLVAVLLVAVLGLEPLRV 300
SLR : 245 QSRGGWLAVLALGATFLALCYFWNLPLQPKFWQWNSLPLAIAVAVILGGGALIAVEPIRL 304

      R +SIF GREDESSNNFRINVLAVLQMIQDRPNLIGPGNTAFNLVPLYQQARFTALSA 360
ICTB : 301 RVLSIFVGREDESSNNFRINVLAVLQMIQDRPNLIGPGNTAFNLVPLYQQARFTALSA 360
SLR : 305 RAMSIFAGREDESSNNFRINVWEGVKAMIRARPIIGIGPGNEAFNQIYPYMRPRFTALSA 364

      YS+ LE+ VE G++G T WLL VT V V R R+ P+ W+M +LA + G+L
ICTB : 361 YSVPLEVAVEGGLGLTAFANLLLVTAVTAVRQVSRRLRRDRNPQAFNLMASLAGLMLG 420
SLR : 365 YSIYLEILVETGVVGFTCMNLNLLAVTLGKGVVELVKRCRQTLAPEGIWMGALAAIIGLLV 424

      HG+ DTV YRP STLWNL + +AS W ++ + B+ D+ +
ICTB : 421 HGLFDTVLYRPERASTLWMLCIGAIASFQWQPQPSKQLPPEAEHSDEKM 467
SLR : 425 HCMVDTVWYRPPVSTLWMLLVAVIVASQWASQAARLBASKEENEDKPL 471

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Fig. 3

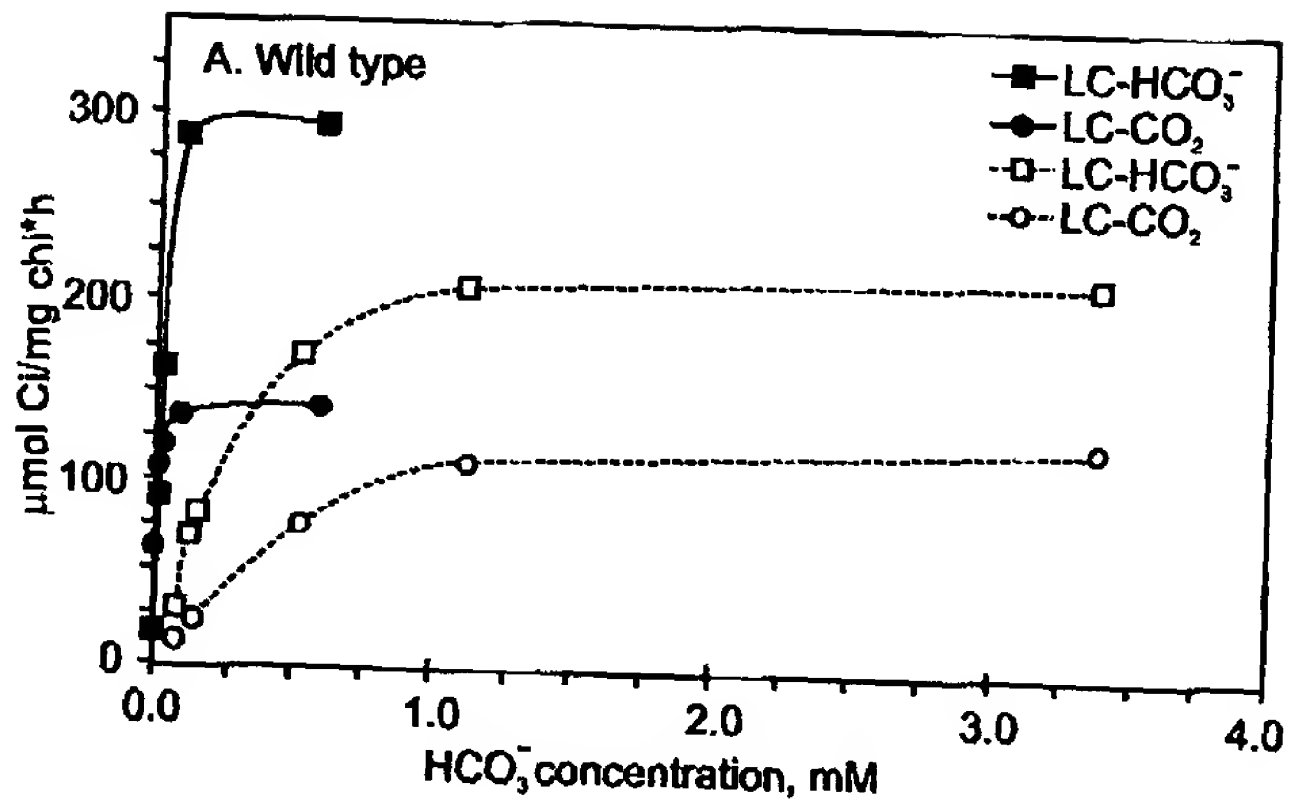


Fig. 4a

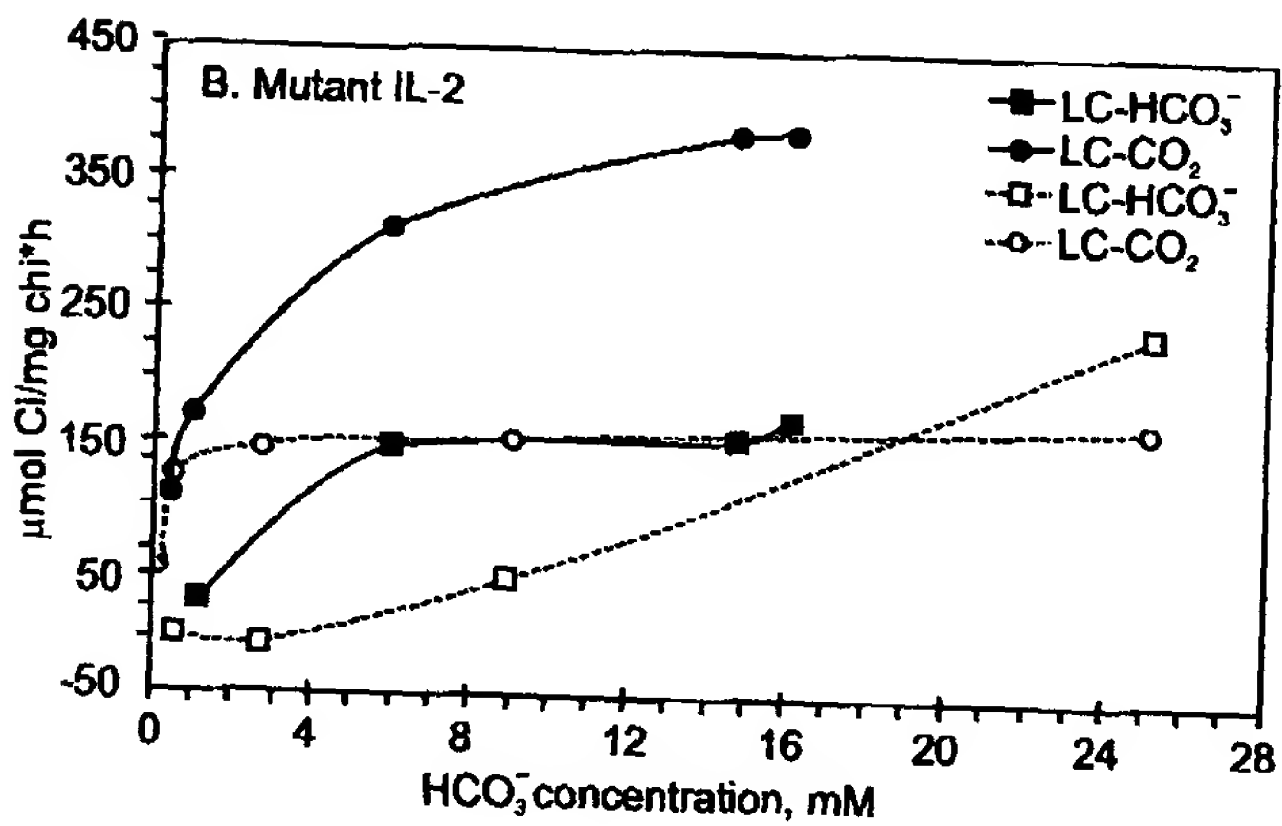


Fig. 4b



Wild type	GGGCT-AGCCGCGATCGCGGCTATTGGGCCC	(SEQ ID NO: 6)
IL-2 ApaI side	GGGCT-AG--G-GATCGC-GCCTATTGGGCCC	(SEQ ID NO: 7)
IL-2 BamHI side	GGGCTCA-----GATCGC-GCCTATTGGGCCC	(SEQ ID NO: 8)
IctB	G L A A I A A Y W A L	(SEQ ID NO: 9)

Fig. 5

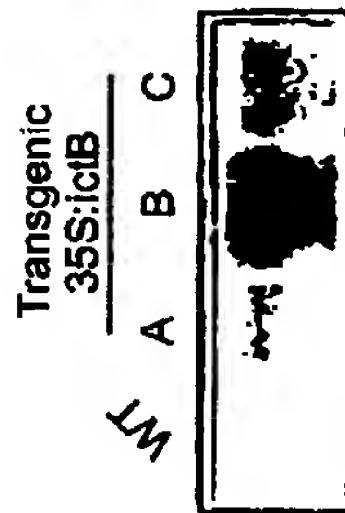


Fig. 6